

- 1 -

piece 1, NC\_000913, nac\_asnV+, config: linear, direction: +, begin: 2059928, end: 2060303

Sequence alignment of nine homologous proteins. The alignment shows the amino acid sequence for each protein, with positions 1 through 20600000 indicated above the sequence. A red dot at position 2059940 indicates a mutation in the S. Infantis protein.

 p35 6.1 bits

ir na c\_a

... ir

第 1 页

p10 1.9 bits

 p35 2.5 bits

 p35 6.1 bit

(6)-ir 2060046 Gap 4.3 bits

} sd-(6)-ir 2060080 Gap 4.3 bit

|-----| sd-ir 2060046 nac\_asnV+ total 5.8 bi  
p10 5.2 bits

```
| sd-ir 2060080 nac_asnV+ total 6.8 bit  
{----- p35-(23)-p10 2
```

```
{-----} p35-(21)-p10 2060034 Gap 3.3 b  
{-----} p35-b10 2060034 total 8.0 bits
```

3 bits  
bits

|----- ... p35-p10 2060104 total 5.5

Sequence alignment diagram showing protein sequences from p35-p10 and p35-p10 2060050. The top row shows the sequence with codons and amino acids. The bottom row shows the sequence with color-coded boxes indicating domains: red for signal peptide, blue for p10, green for p35, and yellow for p35-p10. A dashed box highlights a domain spanning from position 100 to 140.

```
... -----] p35-(23)-p10 2060104 Gap 1.4 bits  
... -----| p35-p10 2060104 total 5.5 bits
```

```
[-----] sd-(6)-ir 2060145 Gap 4.3 bits  
[-----] sd-ir 2060145 nac asnV-total 8.2 bits  
[-----] sd-(16)-ir 2060155 Gap 6.4 bits
```

Sequence alignment diagram showing the nucleotide sequence from position 5' to 206025 across three reading frames. The top row shows the sequence with codons and amino acids. The bottom row shows the sequence with predicted proteins: p35 (6.4 bits), orf 18 codons, p10 (3.8 bits), and p35 (6.4 bits). Colored boxes highlight specific regions: purple for the first p35, green for the orf 18 codons, blue for the second p35, and yellow for the p10 protein.

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18 sedan

**p10** 3.8 bi

புது வரும் p35 6.4 bi

{----- } p35-(21)-p10 2060198 Gap 3.3 bits  
{----- } p35-p10 2060198 total 4.8 bits

{-----} ... p35-(23)-p10 2060261 Gap

